

tetrapeptide or pentapeptide units. The units are derived from units observed to be repeated in the tropoelastin molecule, Val-Pro-Gly-Val-Gly (VPGVG; SEQ ID NO:6) and Val-Pro-Gly-Gly (VPGG; SEQ ID NO:7). The polypeptide comprises a series of beta-turns and is proposed to have a beta-coil structure. The polypeptide provides elastomeric properties to the composite material, but has little structural strength or integrity. The artificial core fiber provides these latter properties to the composite material.

3. At page 3, second full paragraph, please delete the entire paragraph and replace with the following:

Elastin-based materials also have been used to produce solid materials from which prostheses can be manufactured. These include soluble animal elastin co-aggregated with other proteins such as collagen, fibrin, fibronectin and laminin, to produce gel-like materials, and polymerized materials derived from short hydrophobic sequences of human elastin (such as PGVGVA; SEQ ID NO:5). In some cases, these synthetic peptides also include short alanine-rich sequences containing lysine residues, allowing cross-linking between the elastin-like peptides or to other proteins such as collagen. Both elastin and collagen contain crosslinks derived from lysine. For example, U.S. Patent No. 5,223,420 (Rabaud) is directed to an elastin-based product comprising an adduct containing elastin and at least one other protein, such as fibrin.

4. At page 3, line 32 – page 4, line 7, please delete the entire paragraph and replace with the following:

U.S. Patent No. 4,589,882 (Urry) is directed to an artificial elastomeric copolymer comprising an elastomeric component of repeating units of tetrapeptides and pentapeptides and a crosslinking component which may comprise amino acid residues. The repeating units are derived from elastin. U.S. Patent No. 4,132,746 (Urry) is directed to a synthetic, insoluble, crosslinked polypentapeptide. The pentapeptide is the VPGVG (SEQ ID NO:6) peptide present in tropoelastin. See also U.S. Patent No. 4,500,700, U.S. Patent No. 4,870,055, and U.S. Patent No. 5,250,516 (all to Urry) for other materials derived from this peptide. The polypeptides described in these patents comprise a series of beta-turns and are proposed to have a beta-coil structure.

5. At page 6, lines 34-37, please delete the entire paragraph and replace with the following:

Figure 1B shows the amino acid sequence of human elastin (SEQ ID NO:1), without the signal peptide. The underlined amino acid residues comprise the polypeptide of the present invention named MFU-1.

6. At page 7, lines 15-17, please delete the entire paragraph and replace with the following:

Figure 4C shows the amino acid sequence of MFU-2 (SEQ ID NO:2).

7. At page 7, line 21, please insert the following paragraph:

Figures 5A, 5B and 5C show the amino acid sequences of MFU-3 (SEQ ID NO:9), MFU-4 (SEQ ID NO:10), and MFU-5 (SEQ ID NO:11), respectively.

8. At page 8, line 32 – page 9, line 5, please delete the entire paragraph and replace with the following:

Tropoelastin consists predominantly of alternating hydrophobic and crosslinking domains. Indik *et al.*, *Proc. Nat'l Acad. Sci. USA* 84: 5680-84 (1986). Crosslinking domains are rich in alanine (A), with the lysines (K) destined for involvement in crosslink formation present in KAAK (SEQ ID NO:3) and KAAAK (SEQ ID NO:4) spacings. The domains separating these crosslinking regions are strongly hydrophobic in character, and contain many tandemly repeated penta- and hexa-peptide sequences. In human elastin the most striking of these is the sequence PGVGVA (SEQ ID NO:6), repeated 7 times in exon 24. Indik *et al.*, *supra*.

9. At page 9, line 31 – page 10, line 17, please delete the entire paragraph and replace with the following:

As shown in Figure 1A, human elastin consists for most of its length of alternating crosslinking domains and hydrophobic domains. The crosslinking domains consist mainly of lysine (K) and alanine (A) residues in KAAK (SEQ ID NO:3) and KAAAK (SEQ ID NO:4) sequences, wherein the lysine residues are in a suitable conformation for oxidative deamination by lysyl oxidase and subsequent formation of the covalent desmosine crosslinks.

Indik *et al.*, *supra*. The hydrophobic domains are rich in hydrophobic pentapeptide and hexapeptide sequences believed to be in beta-sheet/beta-turn structures. Tamburro *et al.*, ADVANCES IN LIFE SCIENCES 115-27 (1990). These hydrophobic regions are believed to be important to elastin's physical properties of extensibility and elastic recoil, and to the ability of tropoelastin (the monomeric precursor of elastin) to self-aggregate into fibrillar structures. Robson *et al.*, *supra*; Tamburro *et al.*, *supra*. Other proteins capable of self-aggregation and self-alignment into stable fibrillar matrices, including eggshell chorion proteins of insects, spider dragline silk, and lamprin from lamprey cartilage, all possess similar regions of hydrophobic repeat peptides with beta-sheet/beta-turn structures. Hamodrakas *et al.*, *Int. J. Biol. Macromol.* 11: 307-13 (1989); Simmons *et al.*, *Science* 271: 84-87 (1996); Robson *et al.*, *supra*.

10. At page 13, line 23 to page 14, line 16, please delete the entire paragraph and replace with the following:

In accordance with one embodiment of the invention, a polypeptide is provided whose amino acid sequence is a variant of a portion of the amino acid sequence set forth in Figure 1B (SEQ ID NO:1). The amino acid sequence of such a polypeptide corresponds to a portion of the amino acid sequence set forth in Figure 1B (SEQ ID NO:1), wherein the amino acid sequence set forth in the Figure is modified by the addition, deletion, or substitution of from 1 to about 10 amino acid residues, for example, from 1 to about 5 amino acid residues. Such a polypeptide has a secondary structure comprising at least three beta-sheet/beta-turn structures and exhibits the properties of self-alignment described herein. In accordance with another embodiment of the invention, a polypeptide is provided whose amino acid sequence is a variant of the amino acid sequence set forth in Figure 4C (SEQ ID NO:2). The amino acid sequence of such a polypeptide corresponds to a portion of the amino acid sequence set forth in Figure 4C (SEQ ID NO:2), wherein the amino acid sequence set forth in the Figure is modified by the addition, deletion, or substitution of from 1 to about 10 amino acid residues, for example, from 1 to about 5 amino acid residues. Such a polypeptide has a secondary structure comprising at least three beta-sheet/beta-turn structures and exhibits the properties of self-alignment described herein. Polypeptides whose amino acid sequences are variants of the amino acid sequences set forth in Figures 5A-5C (SEQ ID NOS:9-11, respectively) also are encompassed by the present invention. The amino acid sequences of such polypeptides comprise a portion of an amino acid sequence set forth in Figure 5A, 5B or 5C (SEQ ID NOS:9, 10 or 11, respectively),

wherein the amino acid sequence set forth in the Figure is modified by the addition, deletion or substitution of from 1 to about 10 amino acid residues, for example, from 1 to about 5 amino acid residues. Such polypeptides have a secondary structure comprising at least three beta-sheet/beta-turn structures and exhibit the properties of self-alignment discussed herein.

11. At page 14, second full paragraph, please delete the entire paragraph and replace with the following:

The domain structure of human elastin is illustrated in Figure 1A. As shown in this Figure, there are a number of alternating crosslinking and hydrophobic domains. The hydrophobic domains each are believed to comprise a number of beta-sheet/beta-turn-forming sequences. These domains represent probable MFUs of elastin. One of these, used in further experimentation, is designated by the bracket and is named MFU-1 (see Example 1 below). Figure 1B sets forth the amino acid (SEQ ID NO:1) of human elastin. The underlined amino acid residues, residues 374-499, comprise MFU-1. Other MFUs modeled on human elastin include polypeptides comprising amino acid residues 19-160, 188-367 and 607-717, respectively. The amino acid sequence of MFU-3 (SEQ ID NO:9; Fig. 5A) corresponds to that of MFU-1 without the first five amino acid residues. The amino acid sequence of MFU-4 (SEQ ID NO:10; Fig. 5B) corresponds to that of MFU-1 without the first four amino acid residues.

12. At page 14, line 33 – page 15, line 5, please delete the entire paragraph, and replace with the following:

MFUs modeled on human elastin comprise a portion of the amino acid sequence of the tropoelastin molecule (Figure 1B; SEQ ID NO:1) and have at least three beta-sheet/beta-turn structures in their secondary structure. They also may comprise amino acids residues which are capable of participating in crosslinking, such as lysine residues. In one embodiment of the invention, the MFU comprises two amino acid residues capable of participating in crosslinking in such a manner as to form a desmosine-type linkage. For example, the MFU may comprise a KAAK (SEQ ID NO:3) or KAAAK (SEQ ID NO:4) amino acid sequence.

13. At page 15, first full paragraph, please delete the entire paragraph and replace with the following:

In a preferred embodiment, a polypeptide modeled on human elastin consists essentially of a portion of the amino acid sequence set forth in Figure 1B (SEQ ID NO:1). The phrase "A consists essentially of B" herein denotes that A comprises B and possibly other components that do not materially affect the characteristics of the A-B material. For example, a polypeptide consisting essentially of a portion of the amino acid sequence set forth in Figure 1B (SEQ ID NO:1) denotes a polypeptide which comprises a portion of the amino acid sequence set forth in Figure 1B (SEQ ID NO:1) and which also may comprise other amino acid residues that do not materially alter the characteristics of the polypeptide. That is, the polypeptide maintains the characteristics of having at least three beta-sheet/beta-turn structures, and self-aligning in the same manner as tropoelastin peptides.

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prosthesis, including a prosthesis comprising a synthetic material, an animal materials, and/or a metal. The prostheses can be coated with many layers of MFUs. For example, from 1 layer to 500 or more layers of MFU can be coated onto a prosthesis. The MFUs can be crosslinked after being coated onto the prosthesis to improve the permanence of the coating. As used herein, the term prosthesis is meant to encompass any material that is implanted into the body, including material for blood vessel replacement, for tissue replacement (i.e., "filler" material implanted after tissue loss), for heart valve replacement, cloth-like material, stents, and materials for use as coverings for burns or wounds to promote healing.

16. At page 18, second full paragraph, please delete the entire paragraph and insert the following:

Because the MFU's of the present invention are non-thrombogenic, and provide a surface on which endothelial and other cells can adhere and grow, prostheses coated with MFUs are more biocompatible than an uncoated prosthesis. Coating synthetic prosthesis with MFUs modeled on human elastin significantly inhibits platelet binding and activation. Moreover, prostheses coated with MFUs have the advantage over prosthesis coated with animal-derived elastin of containing a human sequence and, hence, being non-immunogenic. Also, the MFUs comprise a defined, homogeneous peptide rather than an undefined mixture of peptides of various sizes, like the animal-derived products previously described.

17. At page 22, second full paragraph, please delete the entire paragraph and replace with the following:

This particular unit was chosen because the flanking hydrophobic exon, exon 24, contains a seven-fold repeat of a PGVGVA (SEQ ID NO:6) sequence which is likely to play a role in elastin alignment and assembly. The importance of this domain is supported by the fact that domains of similar tandem repeats at this site are found in elastins of several species, and by the evidence that synthetic peptides mimicking this hydrophobic repeat sequence self-aggregate to form fibrillar structures. Also, the PGVGVA sequence (SEQ ID NO:6) interacts specifically with an elastin-binding protein, one of the functions of which is to prevent premature intracellular self-aggregation of tropoelastin. Hinek *et al.*, *J. Cell Biol.* 126: 563-73 (1994). This tropoelastin-binding protein has also been shown to inhibit *in vitro* self-aggregation of solubilized elastin fragments (kappa-elastin). Hinek, *Cell Adhesion & Comm.* 2: 1-9 (1994).